

ABSTRACT OF THE DISCLOSURE

Posttranslational modification of histones, in particular acetylation and deacetylation are involved in the regulation of gene expression. Histone deacetylases remove acetyl groups from histone proteins. The present invention is directed to a method of regulating gene expression in a transgenic plant comprising, introducing into a plant a first chimeric nucleotide sequence comprising a first regulatory element in operative association with a coding sequence of interest, and an upstream activating sequence, and a second chimeric nucleotide sequence comprising a second regulatory element in operative association with a nucleotide sequence encoding histone deacetylase and a nucleotide sequence encoding a DNA binding protein, and growing the transgenic plant. Furthermore, a method for regulating gene expression of an endogenous coding sequence of interest, or modifying a developmental, physiological or biochemical pathway in a plant is provided comprising introducing into a plant a chimeric nucleotide sequence comprising a regulatory element in operative association with a nucleotide sequence encoding histone deacetylase fused with a nucleotide sequence encoding a DNA binding protein capable of interacting with an endogenous controlling sequence, for example an upstream activating sequence, and growing the transgenic plant. This invention also relates to novel histone deacetylase obtained from plants, to novel chimeric construct comprising these, or other histone deacetylase, and to transgenic plants, plant cells, or seeds comprising these chimeric constructs.